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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/924,099

DATE: 01/14/2002

TIME: 18:44:07

Input Set : N:\Crf3\RULE60\09924099.raw

Output Set: N:\CRF3\01142002\I924099.raw

1 <110> APPLICANT: NISHIDA, Yoshihiro  
 2 OKURA, Takanori  
 3 TANIMOTO, Tadao  
 4 KURIMOTO, Masashi  
 5 <120> TITLE OF INVENTION: PEPTIDE  
 6 <130> FILE REFERENCE:  
 7 <140> CURRENT APPLICATION NUMBER: US/09/924,099  
 8 <141> CURRENT FILING DATE: 2001-08-08  
 9 <150> PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511  
 W--> 10 <151> PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23  
 11 <150> PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98  
 W--> 12 <151> PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12  
 13 <150> PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98  
 W--> 14 <151> PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22  
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 17 <210> SEQ ID NO: 1  
 18 <211> LENGTH: 108  
 19 <212> TYPE: PRT  
 20 <213> ORGANISM: Mus musculus  
 21 <400> SEQUENCE: 1  
 22 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly  
 23 1 5 10 15  
 24 Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Asp Ile Gly Ser Lys  
 25 20 25 30  
 26 Leu Tyr Trp Leu Gln Gln Glu Pro Asp Gly Thr Phe Lys Arg Leu Ile  
 27 35 40 45  
 28 Tyr Ala Thr Ser Ser Leu Asp Ser Gly Val Pro Lys Arg Phe Ser Gly  
 29 50 55 60  
 30 Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser Ser Leu Glu Ser  
 31 65 70 75 80  
 32 Glu Asp Phe Val Asp Tyr Tyr Cys Leu Gln Tyr Ala Ser Ser Pro Tyr  
 33 85 90 95  
 34 Thr Phe Gly Gly Thr Lys Leu Ala Ile Lys Arg  
 35 100 105  
 37 <210> SEQ ID NO: 2  
 38 <211> LENGTH: 113  
 39 <212> TYPE: PRT  
 40 <213> ORGANISM: Mus musculus  
 41 <400> SEQUENCE: 2  
 42 Glu Ile Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala  
 43 1 5 10 15  
 44 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Asp Tyr  
 45 20 25 30  
 46 Phe Ile Tyr Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile  
 47 35 40 45  
 48 Gly Asp Ile Asp Pro Tyr Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe  
 49 50 55 60

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50      Arg Asp Lys Ala Thr Leu Thr Val Asp Gln Ser Ser Thr Thr Ala Phe
51      65                      70                      75                      80
52      Met His Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
53                      85                      90                      95
54      Ala Arg Gly Leu Arg Phe Trp Gly Gln Gly Thr Leu Val Thr Val Ser
55                      100                      105                      110
56      Ala
58 <210> SEQ ID NO: 3
59 <211> LENGTH: 11
60 <212> TYPE: PRT
61 <213> ORGANISM: Mus musculus
62 <400> SEQUENCE: 3
63      Arg Ala Ser Gln Asp Ile Gly Ser Lys Leu Tyr
64      1                      5                      10
66 <210> SEQ ID NO: 4
67 <211> LENGTH: 7
68 <212> TYPE: PRT
69 <213> ORGANISM: Mus musculus
70 <400> SEQUENCE: 4
71      Ala Thr Ser Ser Leu Asp Ser
72      1                      5
74 <210> SEQ ID NO: 5
75 <211> LENGTH: 9
76 <212> TYPE: PRT
77 <213> ORGANISM: Mus musculus
78 <400> SEQUENCE: 5
79      Leu Gln Tyr Ala Ser Ser Pro Tyr Thr
80      1                      5
82 <210> SEQ ID NO: 6
83 <211> LENGTH: 10
84 <212> TYPE: PRT
85 <213> ORGANISM: Mus musculus
86 <400> SEQUENCE: 6
87      Gly Tyr Ser Phe Thr Asp Tyr Phe Ile Tyr
88      1                      5                      10
90 <210> SEQ ID NO: 7
91 <211> LENGTH: 17
92 <212> TYPE: PRT
93 <213> ORGANISM: Mus musculus
94 <400> SEQUENCE: 7
95      Asp Ile Asp Pro Tyr Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe Arg
96      1                      5                      10                      15
97      Asp
99 <210> SEQ ID NO: 8
100 <211> LENGTH: 4
101 <212> TYPE: PRT
102 <213> ORGANISM: Mus musculus
103 <400> SEQUENCE: 8
104      Gly Leu Arg Phe

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105      1
107 <210> SEQ ID NO: 9
108 <211> LENGTH: 237
109 <212> TYPE: PRT
110 <213> ORGANISM: Artificial Sequence
111 <220> FEATURE:
112 <223> OTHER INFORMATION: Artificially produced peptide in the form of a single
113 chain
114 variable region fragment (scFv) which neutralizes IL-18
115 <400> SEQUENCE: 9
116 Glu Ile Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
117      1           5           10           15
118 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Asp Tyr
119           20           25           30
120 Phe Ile Tyr Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
121           35           40           45
122 Gly Asp Ile Asp Pro Tyr Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
123           50           55           60
124 Arg Asp Lys Ala Thr Leu Thr Val Asp Gln Ser Ser Thr Thr Ala Phe
125           65           70           75           80
126 Met His Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
127           85           90           95
128 Ala Arg Gly Leu Arg Phe Trp Gly Gln Gly Thr Leu Val Thr Val Ser
129           100          105          110
130 Ala Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
131           115          120          125
132 Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
133           130          135          140
134 Leu Gly Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Asp Ile Gly
135          145          150          155          160
136 Ser Lys Leu Tyr Trp Leu Gln Gln Glu Pro Asp Gly Thr Phe Lys Arg
137           165          170          175
138 Leu Ile Tyr Ala Thr Ser Ser Leu Asp Ser Gly Val Pro Lys Arg Phe
139           180          185          190
140 Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser Ser Leu
141           195          200          205
142 Glu Ser Glu Asp Phe Val Asp Tyr Tyr Cys Leu Gln Tyr Ala Ser Ser
143          210          215          220
144 Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Ala Ile Lys
145          225          230          235
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148 <211> LENGTH: 243
149 <212> TYPE: PRT
150 <213> ORGANISM: Artificial Sequence
151 <220> FEATURE:
152 <223> OTHER INFORMATION: Artificially produced peptide in the form of a single
153 chain
154 variable region fragment (scFv) which neutralizes IL-18
155 <400> SEQUENCE: 10

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156   Glu Ile Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
157       1           5           10           15
158   Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Asp Tyr
159           20           25           30
160   Phe Ile Tyr Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
161           35           40           45
162   Gly Asp Ile Asp Pro Tyr Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
163       50           55           60
164   Arg Asp Lys Ala Thr Leu Thr Val Asp Gln Ser Ser Thr Thr Ala Phe
165       65           70           75           80
166   Met His Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
167           85           90           95
168   Ala Arg Gly Leu Arg Phe Trp Gly Gln Gly Thr Leu Val Thr Val Ser
169           100          105          110
170   Ala Gly Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
171           115          120          125
172   Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
173       130          135          140
174   Leu Gly Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Asp Ile Gly
175       145          150          155          160
176   Ser Lys Leu Tyr Trp Leu Gln Gln Glu Pro Asp Gly Thr Phe Lys Arg
177           165          170          175
178   Leu Ile Tyr Ala Thr Ser Ser Leu Asp Ser Gly Val Pro Lys Arg Phe
179           180          185          190
180   Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser Ser Leu
181           195          200          205
182   Glu Ser Glu Asp Phe Val Asp Tyr Tyr Cys Leu Gln Tyr Ala Ser Ser
183       210          215          220
184   Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Ala Ile Lys His His His
185       225          230          235          240
186   His His His
188 <210> SEQ ID NO: 11
189 <211> LENGTH: 324
190 <212> TYPE: DNA
191 <213> ORGANISM: Mus musculus
192 <400> SEQUENCE: 11
193   gac atc cag atg acc cag tct cca tcc tcc tta tct gcc tct ctg gga 48
194   Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
195       1           5           10           15
196   gaa aga gtc agt ctc act tgt cgg gca agt cag gac att ggt agt aaa 96
197   Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Asp Ile Gly Ser Lys
198           20           25           30
199   tta tac tgg ctt caa cag gaa cca gat gga act ttt aaa cgc ctg atc 144
200   Leu Tyr Trp Leu Gln Gln Glu Pro Asp Gly Thr Phe Lys Arg Leu Ile
201           35           40           45
202   tac gcc aca tcc agt tta gat tct ggt gtc ccc aag agg ttc agt ggc 192
203   Tyr Ala Thr Ser Ser Leu Asp Ser Gly Val Pro Lys Arg Phe Ser Gly
204       50           55           60
205   agt agg tct ggg tca gat tat tct ctc acc atc agc agc ctt gag tct 240

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206 Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser Ser Leu Glu Ser
207 65 70 75 80
208 gaa gat ttt gta gac tat tac tgt cta caa tat gct agt tct ccg tac 288
209 Glu Asp Phe Val Asp Tyr Tyr Cys Leu Gln Tyr Ala Ser Ser Pro Tyr
210 85 90 95
211 acg ttc gga ggg ggg acc aag ctg gca ata aaa cgg 324
212 Thr Phe Gly Gly Gly Thr Lys Leu Ala Ile Lys Arg
213 100 105
215 <210> SEQ ID NO: 12
216 <211> LENGTH: 339
217 <212> TYPE: DNA
218 <213> ORGANISM: Mus musculus
219 <400> SEQUENCE: 12
220 gag atc cag ctg cag cag tct gga cct gag ctg gtg aag cct ggg gct 48
221 Glu Ile Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
222 1 5 10 15
223 tca gtg aag gtc tcc tgt aag gct tct ggt tac tca ttc act gac tac 96
224 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Asp Tyr
225 20 25 30
226 ttc att tac tgg gtg aag cag agc cat gga aag agc ctt gag tgg att 144
227 Phe Ile Tyr Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
228 35 40 45
229 gga gat att gat cct tat aat ggt gat act agt tac aac cag aag ttc 192
230 Gly Asp Ile Asp Pro Tyr Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
231 50 55 60
232 agg gac aag gcc aca ttg act gtt gac cag tcc tcc acc aca gcc ttc 240
233 Arg Asp Lys Ala Thr Leu Thr Val Asp Gln Ser Ser Thr Thr Ala Phe
234 65 70 75 80
235 atg cat ctc aac agc ctg aca tct gag gac tct gca gtc tat ttc tgt 288
236 Met His Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
237 85 90 95
238 gca aga ggc cta cgg ttc tgg ggc caa ggg act ctg gtc act gtc tct 336
239 Ala Arg Gly Leu Arg Phe Trp Gly Gln Gly Thr Leu Val Thr Val Ser
240 100 105 110
241 gca 339
242 Ala
244 <210> SEQ ID NO: 13
245 <211> LENGTH: 33
246 <212> TYPE: DNA
247 <213> ORGANISM: Mus musculus
248 <400> SEQUENCE: 13
249 cgg gca agt cag gac att ggt agt aaa tta tac 33
250 Arg Ala Ser Gln Asp Ile Gly Ser Lys Leu Tyr
251 1 5 10
253 <210> SEQ ID NO: 14
254 <211> LENGTH: 21
255 <212> TYPE: DNA
256 <213> ORGANISM: Mus musculus
257 <400> SEQUENCE: 14

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## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/924,099

DATE: 01/14/2002

TIME: 18:44:08

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L:14 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD  
L:408 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:20  
L:429 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
L:459 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:524 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27  
L:563 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:28